

# SURFACE-MEDIATED ACTIVATION OF BLOOD COAGULATION (INTRINSIC SYSTEM)

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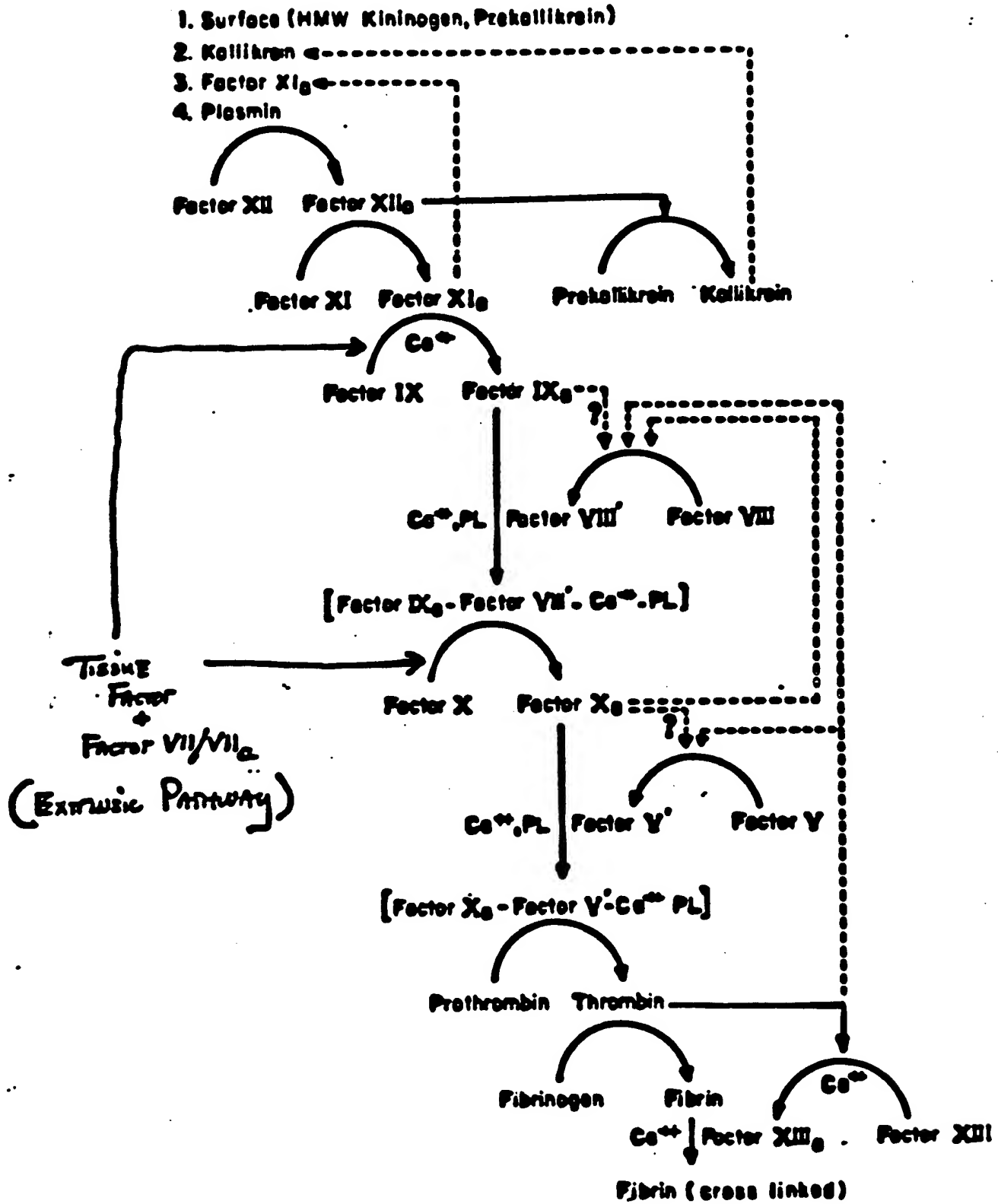
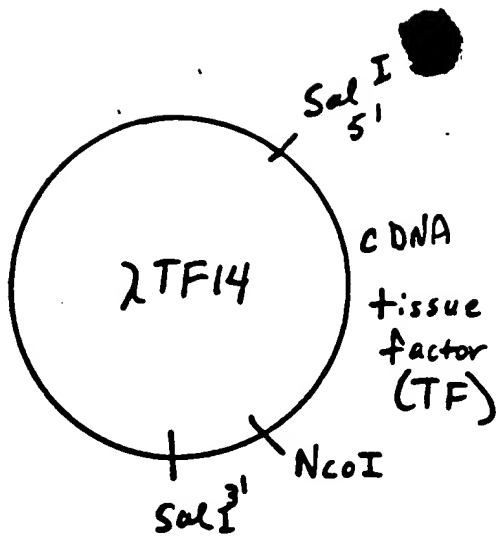


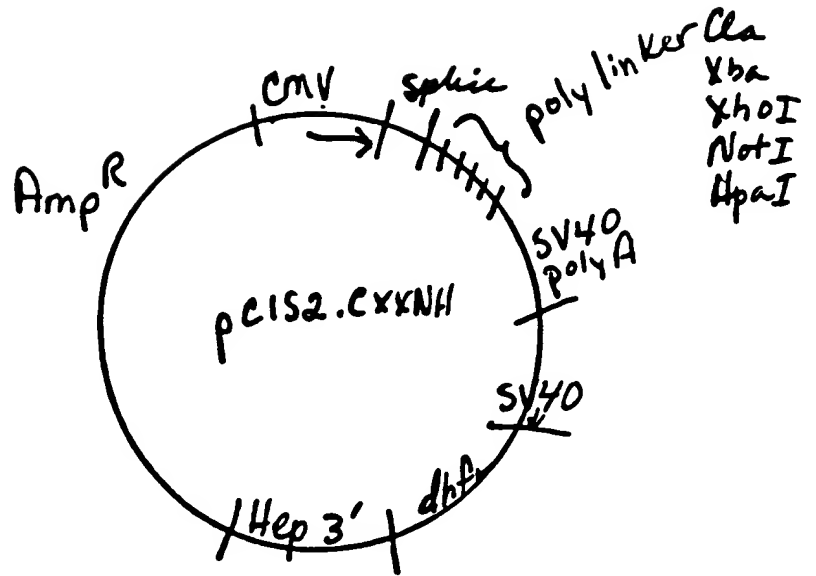
FIGURE 1

FIGURE 4

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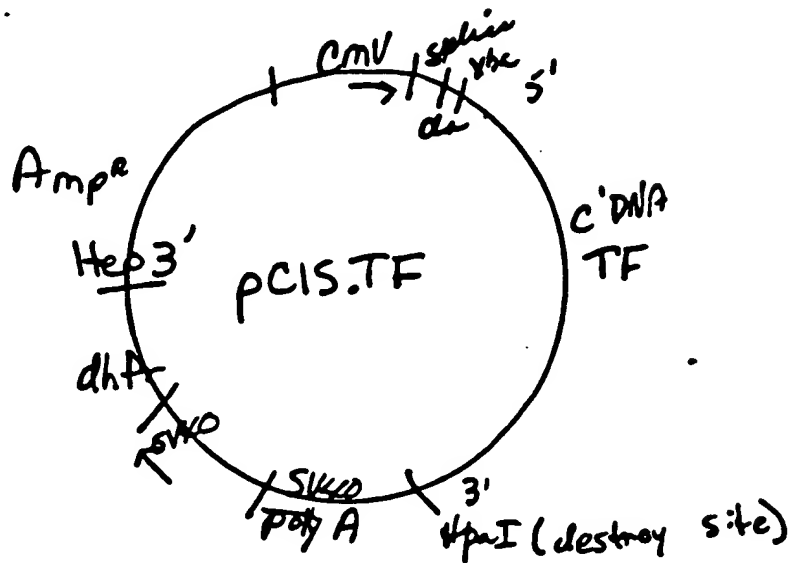
1. cut with NcoI
2. fill in with Klenow  
+ 4 dNTP
3. cut with Sal (TCGA)
4. isolate 1232 bp fragment



1. cut with XhoI (TCGA)  
and HpaI
2. gel purify



ligation



1 CTCGCACTCCCTCTGCGCGGCCACGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGAC  
100 ATG GAG ACC CCT GCC TGG CCC CGG GTC CCG CGC CCC GAG ACC GCC GTC GCT CGG ACG CTC CTG CTC GGC TGG GTC  
-32 Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val Ala Arg Thr Leu Leu Leu Gly Trp Val  
175 TTC GCC CAG GTG GCC GGC GCT TCA GGC ACT ACA AAT ACT GTG GCA GCA TAT AAT TTA ACT TGG AAA TCA ACT AAT  
-7 Phe Ala Gln Val Ala Gly Ala Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn  
250 TTC AAG ACA ATT TTG GAG TGG GAA CCC AAA CCC GTC AAT CAA GTC TAC ACT GTT CAA ATA AGC ACT AAG TCA GGA  
19 Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly  
325 GAT TGG AAA AGC AAA TGC TTT TAC ACA ACA GAC ACA GAG TGT GAC CTC ACC GAC GAG ATT GTG AAG GAT GTG AAG  
44 Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys  
400 CAG ACG TAC TTG GCA CGG GTC TTC TCC TAC CCG GCA GGG AAT GTG GAG AGC ACC GGT TCT GCT GGG GAG CCT CTG  
69 Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu  
475 TAT GAG AAC TCC CCA GAG TTC ACA CCT TAC CTG GAG ACA AAC CTC GGA CAG CCA ACA ATT CAG AGT TTT GAA CAG  
94 Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln  
550 GTG GGA ACA AAA GTG AAT GTG ACC GTA GAA GAT GAA CGG ACT TTA GTC AGA AGG AAC AAC ACT TTC CTA AGC CTC  
119 Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu  
625 CGG GAT GTT TTT GGC AAG GAC TTA ATT TAT ACA CTT TAT TAT TGG AAA TCT TCA AGT TCA GGA AAG AAA ACA GCC  
144 Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala  
700 AAA ACA AAC ACT AAT GAG TTT TTG ATT GAT GTG GAT AAA GGA GAA AAC TAC TGT TTC AGT GTT CAA GCA GTG ATT  
169 Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile  
775 CCC TCC CGA ACA GTT AAC CGG AAG AGT ACA GAC AGC CCG GTA GAG TGT ATG GGC CAG GAG AAA GGG GAA TTC AGA  
174 Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg  
850 GAA ATA TTC TAC ATC ATT GGA GCT GTG GTA TTT GTG GTC ATC ATC CTT GTC ATC ATC CTG GCT ATA TCT CTA CAC  
219 Glu Ile Phe Tyr Ile Ile Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile Ser Leu His  
925 AAG TGT AGA AAG GCA GGA GTG GGG CAG AGC TGG AAG GAG AAC TCC CCA CTG AAT GTT TCA TAA AGGAAGCACTGTTGG  
244 Lys Cys Arg Lys Ala Gly Val Gly Gln Ser Trp Lys Glu Asn Ser Pro Leu Asn Val Ser End  
1003 AGCTACTGCAAAATGCTATATTGCACTGTGACCGAGAACCTTTAAGAGGATAGAATACATGGAACGCAAAATGAGTATTTGCGAGCATGAAGACCCCTGGAG  
1103 TTCAAAAACTCTTGATATGACCTGTTATTACCATTAGCATTCTGGTTTTGACATCAGCATTAGTCACTTTGAAATGTAACGAATGGTACTACAACCAAT  
1203 TCCAAGTTTTAATTTTTAACACCATGGCACCCTTTGACATAACATGCTTTAGATTATATATTCGCACTCAAGGAGTAACAGGTCGTCCAAGCAAAAA  
1303 CAAATGGGAAAATGTCTTAAAAAATCCTGGGTGGACTTTTGAAGCTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTTGCTCTGTTGCCAGGCTGGA  
1403 GTGAGTAGCACGATCTCGGCTCACTGCACCTCCGCTCTCGGGTTCAAGCAATTGCTGCTCAGCTCCCGAGTAGCTGGGATTACAGGTGC6CACT  
1503 ACCACACCAAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTACCATCTTG6CCAGGCTGGTCTTGAATTCCTGACCTCAGTTGATCCACCCACCT  
1603 TGGCTCCCAAAGTGTAGTATTATGGGCTGAACCATGCCCAGCCGAAAAGCTTTTGAAGGGCTGACTTCAATCCATGTAGGAAAGTAAATGGA  
1703 GGAATTTGGGTGATTTCTAGGACTTTTCTAACATATGCTATAATATAGTGTGTTAGGTTCTTTTTTTTTTTCAGGAATACATTTGGAATTCAAAACAA  
1803 TGGCAAACTTTGTATTAATGTGTTAAGTGCAAGGACATTGGTATTCTGGGCACCTTCTTAATATGCTTTACAATCTGCACTTTAACTGACTTAAGTGGC  
1903 ATTAACATTTGAGAGCTAACTATATTTTATAAGACTACTATACAACTACAGAGTTTATGATTTAAGGACTTAAAGCTTCTATGGTTGACATTGTAT  
2003 ATATAATTTTTTAAAAAGGTTTTCTATATGGGGATTTTCTATTTATGTAGGTAATATTGTTCTATTTGTATATATTGAGATAATTTATTTAATATACTTT  
2103 AAATAAAGGTGACTGGGAATTGTTA<sub>n</sub>

[illegible]

1001 GGAGCTACTG CAAATGCTAT ATTGACTGT GACCGAGAC TTUATAGAG ATGAGATACA TGGAAAGCA ATGAGATAT TCCGACGATG AAGACTGTG  
CCTGATGTAC GTTATACATA TAACTGACA CTGGCTGTG AATATCTG TATCTATGT ACCCTTGGT TATCTATTA AGCTCTGAC TTCTGGAC

1101 AGTCAAAA ACTCTGATA TGACTGTATA TTACATTAG CATCTGTGT TTGACATGAC CATATGTAC TTGGAATGT AACGAATGT ACTACACCA  
TCAAGTTT TGAACATAT ACTGACAT ATGTGTATC GTAAAGCCA AACTGTAGT GTATGTAGT AACTTACA TTCTTACA TGAATGTAT

1201 ATTCCAGT TTAATTTTA ACACATGCT ACCCTTGCA CATACATGC TTATGATAT ATATGCGA CTCAAGACT AACGAGTGC TCGAACAAA  
TAACTTCA ATTAAAT TGTGTATCG TCGAAAGCT GTATGTAGT AATCTATA TATAGCGT GAGTGTCTA TTGTGCGC AGCTCTT

1301 AACAAATGG AATGTCTT AAAAATCT GCGTGACTT TGAATAGT TTTTCTT TTTTCTT AGACGAGTGT TTGCTGTGT GCCACGCTG  
TTGTATCC TTATACGA TTTTACA CCGACTGTA AACTTCA AAAAAAA AAAAAAA TCTGCTGAC AACGACAA CCGCTCGAC

1401 GAGTGCAT GACATGCT GCGTACATG ACCCTCGCT TCTGAGGTG AACGAATGT CTGCGTAG CTCCGAGTA CTGAGATTA CAGTGCCTA  
CTACGCTAT CTCTAGAG CCGATGACG TCGAGGCGAG AAGGCCAAG TTCTTACA GACGAGTGT GAGGCTCAT CACCTTAT GTCCACGCT

1501 CTACGACAG AAGCAATTT TTGATTTT TATGAGAGT GCGGTTCAC GAGTTCAC CATCTGCG CAGCTGCT TCAATCTGT AACTGATG ATCCACGAC  
CATGCTGTG TTCAATTA AACATAAA ATCATCTTA CCGCAAGTG GTAGAACCG TCCGACGCA ACTTAAGAC TGAATGCAC TATGTGCTG

1601 CTGGCTCG CAAATGCTA GTATTATGG CCGTACGAC CATGCGCAG CCAAACTT TTGAGGCT GACTCAATG CATGAGGAA AGTAAATG  
GAACGAGAG GTTACATAT CATATACCC CCACTTGTG TATGCTGTG CTTTCTGA AATCCCGCA CTGAATGAT GTACTCTT TCAATTACC

1701 AAGCAATG GGTCAATTC TAGCACTTT CTAACTATG TCAATATAT AGCTTATG TTCTTTT TTCAAGAT ACATTTGAA ATTCAACA  
TTCTTTAC CCACTAAG ATCTGAAA GATGTATAC AATATATA TCAAAATC AAAAAAA AAGTCTTA TGTAACTT TAACTTGT

1801 ATTGCAAC TTGTATTA TGTGTATG GCAGGAGCA TTGTATTC GCGACTCT CTATATGT TTCAATGT TACATGTG CACTTACT GACTAATG  
TAACTGTG AACATATT ACATATTC CCGCTGTGT AACATACA CCGGTGAG GATTATGCA AATGTAGC GTCAATTGA CTGAATGAC

1901 GCAATTAACA TTGAGACT AACTATAT TATAAGAT ACTATACAA CTACAGAT TATGATTA TATGATTA GATATTA GCTGTATG TGAATGT  
CGTAATGT AACTGTCA TGAATATA ATATCTGA TGAATGTG GATGTCA ATCTAAT CCAATATT CCAAGATG AACTTACA

2001 ATATATAT TTTAATAG GTTCTTATA TCGGATTT CTATTATG AGGTATGT GTCTATTT GTCTATTT TATATGCA GATATTA TTAATAT  
TATATATTA AATTTTC CAAAGATAT ACCCTAAA GATATACA TCAATTTA CAAGATAC ATATATAT GATATTA ATATAT

2101 TTAATTAAG GTGACTGCA ATTGTA  
AATTAATTC CACTGACCT TAACAT

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Fig. 5

